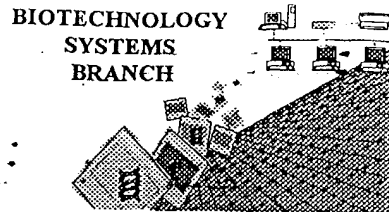


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/674,124
Source: 0.72
Date Processed by STIC: 10-8-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office.
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/674,124

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



II

RAW SEQUENCE LISTING

DATE: 10/08/2003

PATENT APPLICATION: US/10/674,124

TIME: 13:16:54

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

3 <110> APPLICANT: INOKO, Hidetoshi
 4 TAMIYA, Gen
 7 <120> TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
 8 GENETIC POLYMORPHISM MARKERS
 11 <130> FILE REFERENCE: TECH-003CIP
 > 13 <140> CURRENT APPLICATION NUMBER: US/10/674,124
 14 <141> CURRENT FILING DATE: 2003-09-26
 16 <150> PRIOR APPLICATION NUMBER: 10/257,511
 17 <151> PRIOR FILING DATE: 2003-03-07
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP00/07621
 20 <151> PRIOR FILING DATE: 2000-10-30
 22 <150> PRIOR APPLICATION NUMBER: JP2000-112699
 23 <151> PRIOR FILING DATE: 2000-04-13
 25 <150> PRIOR APPLICATION NUMBER: JP2002-327516
 26 <151> PRIOR FILING DATE: 2002-09-28
 28 <150> PRIOR APPLICATION NUMBER: JP2002-383869
 29 <151> PRIOR FILING DATE: 2002-12-09
 31 <160> NUMBER OF SEQ ID NOS: 27110
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 466
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Homo sapiens
 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: chr8.fa.07frz.212765
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Located on chromosome 1
 44 <220> FEATURE:
 45 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
 46 chromosomal short arm and 5'-terminus of this base
 47 sequence : 8211
 49 <220> FEATURE:
 50 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
 51 sequence listing upward to telomere on chrosomal short arm and
 52 5'-terminus of this base sequence : 0
 54 <400> SEQUENCE: 1
 55 agatggatga tagatcattg atagatgata ggtagatagt agatagatta taggtagata 60
 57 aatagatgga tgatggatgg atgatagata cttgattgat agatgatagg tagatagtag 120
 59 atagatgata gataatgata gatgatagct agatagtaga tagatgtgat aggtagatgg 180
 61 tagatagaga tgatgataga tggatgatag atggatggat ggatgatagg tgattgatag 240
 63 atggtagata ggtggatggt agagatggta gataaataga tggatgatgg atggatgata 300
 65 gagagctgat agtagataag gtagatagta gatagatgat agatggatgg atgatagatg 360
 67 attgatagag agatagagag agaaggatga tagactgagc atcataactt cactgaatgc 420
 69 taccagttgg attcaaaagt cagcaaactg aaacgtcgaa tttcag 466

P.6
 Does Not Comply
 Corrected Diskette Needed

RAW SEQUENCE LISTING

DATE: 10/08/2003

PATENT APPLICATION: US/10/674,124

TIME: 13:16:54

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

```

72 <210> SEQ ID NO: 2
73 <211> LENGTH: 207
74 <212> TYPE: DNA
75 <213> ORGANISM: Homo sapiens
77 <220> FEATURE:
78 <223> OTHER INFORMATION: DISD22_0011793
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Located on chromosome 1
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
85     chromosomal short arm and 5'-terminus of this base
86     sequence : 100269
88 <220> FEATURE:
89 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
90     sequence listing upward to telomere on chrosomal short arm and
91     5'-terminus of this base sequence : 91592
93 <400> SEQUENCE: 2
94 aaccagtgtct tagcagacgc cgtccctcag gatgcaggca cacgcacaca cacacacaca      60
96 cacatgcaca cgcacacaca tgaacacaca tggacacgcg aacacacaca tgcacacgta      120
98 cacacgtgtg ctgacacgcg gatgctgggc cagggctcac cactccaacg cgggggtcctg      180
100 gcagcccagc gggtagcaga gctcaat                                     207
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 271
105 <212> TYPE: DNA
106 <213> ORGANISM: Homo sapiens
108 <220> FEATURE:
109 <223> OTHER INFORMATION: DIS07_10007615
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Located on chromosome 1
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
116     chromosomal short arm and 5'-terminus of this base
117     sequence : 706251
119 <220> FEATURE:
120 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
121     sequence listing upward to telomere on chrosomal short arm and
122     5'-terminus of this base sequence : 605775
124 <400> SEQUENCE: 3
125 tgtgaacttc aaactctcag gggttttctga ggaataaaga ggggtttttgc aaaatggagt      60
127 cagggtcgcc ttctgttttt tctttctttc tttctttctt tttttttttt ttgagaagga      120
129 gcctcgctct gtccaaggt tggagtgcaa tggcaggatc ttggctcact gcaacctctg      180
131 cctcccgggt tcaagtgatt ctctacctct gcctcctgag tagctgggac tacaagcacg      240
133 tgccatgtgt agagatggca tctcactgtg t                                     271
136 <210> SEQ ID NO: 4
137 <211> LENGTH: 123
138 <212> TYPE: DNA
139 <213> ORGANISM: Homo sapiens
141 <220> FEATURE:
142 <223> OTHER INFORMATION: DIS07_10000554

```

RAW SEQUENCE LISTING

DATE: 10/08/2003

PATENT APPLICATION: US/10/674,124 TIME: 13:16:54

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

```

144 <220> FEATURE:
145 <223> OTHER INFORMATION: Located on chromosome 1
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
149     chromosomal short arm and 5'-terminus of this base
150     sequence : 1020587
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
154     sequence listing upward to telomere on chrosomal short arm and
155     5'-terminus of this base sequence : 314065
157 <400> SEQUENCE: 4
158 acgcagattg gtctgtcccc agagggcgct tggagggcag cggaaggatt cgggcctgga      60
160 taggggcttg acctagccct cctcctcctc ctctcctcc tctcgaagt gggcttgctt      120
162 ctt                                                                    123
165 <210> SEQ ID NO: 5
166 <211> LENGTH: 410
167 <212> TYPE: DNA
168 <213> ORGANISM: Homo sapiens
170 <220> FEATURE:
171 <223> OTHER INFORMATION: chr1.fa.07frz.1780396
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Located on chromosome 1
176 <220> FEATURE:
177 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
178     chromosomal short arm and 5'-terminus of this base
179     sequence : 1105774
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
183     sequence listing upward to telomere on chrosomal short arm and
184     5'-terminus of this base sequence : 85064
186 <400> SEQUENCE: 5
187 gctaaactttc atcttttagtc acatgcaaag agaaaaaac cagacggact tctttttcat      60
189 agttaatatgc agaaattatt atagcactct gctgtgcaa catttgagtt tcaattcaga      120
191 gactcaaaac ctacgtttgt caattttttt taaaaaggcg tattcctggc tgggcatggg      180
193 gggctataat cccaacactt taggagggtca agtcgggagg actgcttgaa tccagcagtt      240
195 tgcgaccagc ctgggcaata tggcaaaacg ctgtgtacac acacacatac acacatacac      300
197 acacacacac acacaatttt tgtttagcaat aaaaataaat ttcttggtca ggccctcttc      360
199 agtcacacac tagaagtgat aagaaaaatc tattgtcagg catttcaatt      410
202 <210> SEQ ID NO: 6
203 <211> LENGTH: 102
204 <212> TYPE: DNA
205 <213> ORGANISM: Homo sapiens
207 <220> FEATURE:
208 <223> OTHER INFORMATION: DISD22_0011809
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Located on chromosome 1
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
215     chromosomal short arm and 5'-terminus of this base

```

RAW SEQUENCE LISTING

DATE: 10/08/2003

PATENT APPLICATION: US/10/674,124

TIME: 13:16:54

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

```

216     sequence : 1238096
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
220     sequence listing upward to telomere on chrosomal short arm and
221     5'-terminus of this base sequence : 131912
223 <400> SEQUENCE: 6
224 cagaggacgc agagctaaga aagttgggac cttttttttt tcagcactac acacacacac      60
226 acacacacga actgcagggg gctctggagc catggagtta ga      102
229 <210> SEQ ID NO: 7
230 <211> LENGTH: 162
231 <212> TYPE: DNA
232 <213> ORGANISM: Homo sapiens
234 <220> FEATURE:
235 <223> OTHER INFORMATION: D1S243
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Located on chromosome 1
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
242     chromosomal short arm and 5'-terminus of this base
243     sequence : 1525955
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
247     sequence listing upward to telomere on chrosomal short arm and
248     5'-terminus of this base sequence : 287757
250 <400> SEQUENCE: 7
251 gctccagcgt catggacttt tccggccttg ggtcgaggcc tcagcgattc aggcggggcc      60
253 gtttttgtaa cacccggtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg      120
255 tccgtgcgcg cgcgcgatgc tgcaggcatg tgagcctgtg tg      162
258 <210> SEQ ID NO: 8
259 <211> LENGTH: 283
260 <212> TYPE: DNA
261 <213> ORGANISM: Homo sapiens
263 <220> FEATURE:
264 <223> OTHER INFORMATION: DIS07_10007619
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Located on chromosome 1
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
271     chromosomal short arm and 5'-terminus of this base
272     sequence : 1667184
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
276     sequence listing upward to telomere on chrosomal short arm and
277     5'-terminus of this base sequence : 141067
279 <400> SEQUENCE: 8
280 ctgtcacoga gaagggacct gggctggcct ttcctttgcc tttttaaata ttttatttta      60
282 ttttatatatt tattttatatt tattttatatt tatttatatt attttatttt attttatttt      120
284 attttatttt attttatttt aatcatagag atggggcctc cctttgtggc ccaggctggc      180
286 cttgaactcc tgagttcaag caatcctccc gcctcagcct cccaaagtgc tgggatcacg      240

```

RAW SEQUENCE LISTING

DATE: 10/08/2003

PATENT APPLICATION: US/10/674,124

TIME: 13:16:54

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

```

288 ggcgtggccc cgcgccagct cccctgcctt tcttgaggca tag .. 283
291 <210> SEQ ID NO: 9
292 <211> LENGTH: 260
293 <212> TYPE: DNA
294 <213> ORGANISM: Homo sapiens
296 <220> FEATURE:
297 <223> OTHER INFORMATION: DISD22_0011823
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Located on chromosome 1
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
304 chromosomal short arm and 5'-terminus of this base
305 sequence : 2173981
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
309 sequence listing upward to telomere on chrosomal short arm and
310 5'-terminus of this base sequence : 506514
312 <400> SEQUENCE: 9
313 tccatcagtc tagctggaag attttagtta aaaaaaggct gtgtgtgtgt gtgtgtgtgt 60
315 gtgtgtgtgt gtgtgtgtgt gtctgtctgt ctgtctgtct gtctgcctag gtagatggat 120
317 ggagaaatgg gcggatggat gaatgggtgg atggatggat agatggatag atgaatgaat 180
319 ggacagatgg atatgtgagt gtgtgtgtgt gtgtgtgtct gtgtctgtct gtctgtctag 240
321 gtagtcagat ggataaatgc 260
324 <210> SEQ ID NO: 10
325 <211> LENGTH: 142
326 <212> TYPE: DNA
327 <213> ORGANISM: Homo sapiens
329 <220> FEATURE:
330 <223> OTHER INFORMATION: DISD22_0011835
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Located on chromosome 1
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Distance between a terminus base of telomere on
337 chromosomal short arm and 5'-terminus of this base
338 sequence : 2407733
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
342 sequence listing upward to telomere on chrosomal short arm and
343 5'-terminus of this base sequence : 233492
345 <400> SEQUENCE: 10
346 gaaattaggt caagacgtat gcatgtgcgt gtttgtgtgt gtgtgtgtgt gtgtgtgtgt 60
348 gtgttggttt attgctcatg aaagcagatt tgaatttctt ttaagagtgt agccaattct 120
350 ctcatatatcc aactcagttt cc 142
353 <210> SEQ ID NO: 11
354 <211> LENGTH: 245
355 <212> TYPE: DNA
356 <213> ORGANISM: Homo sapiens
358 <220> FEATURE:
359 <223> OTHER INFORMATION: DIS07_10007628

```

<210> 27089

<211> 28

<212> DNA

<213> Artificial

See page 8 on error
summary report

<400> 27089

aatagccatg agaagctatg tgggggag

28

<210> 27090

<211> 29

<212> DNA

<213> Artificial

<400> 27090

ctacctcctt gccaaacttg ctgtttgtg

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

<210> 863
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<223> DISD22_0000537

<220>
<223> Located on chromosome 1

<220>
<223> Distance between a terminus base of telomere on
chromosomal short arm and 5'-terminus of this base
sequence : 90759656

<220>
<223> Distance between 3'-terminus of neighbour sequence of
sequence listing upward to telomere on chrosomal short arm and
5'-terminus of this base sequence : 295398

<400> 863
ttctccttca gaccctctga aaaaaaatgt tacctttttg aggatggctc tctatttttt 60
tctccctagc ccctatgttt taaaaaagct aagcgtgtgt gtgtgtgtgt gtgtgtgtgt 120
gtgtgtgtgt gtgtgtgttt tgaagggagc aggcacaaaa gggaggggag tggaaagtaa 180
ttattatcat cccaacgtct t 201

NO explanation given for "n"
See item 9 on error summary
sheet.

<210> 912
 <211> 259
 <212> DNA
 <213> Homo sapiens

<220>
 <223> AL157410.5_47389

<220>
 <223> Located on chromosome 1

<220>
 <223> Distance between a terminus base of telomere on
 chromosomal short arm and 5'-terminus of this base
 sequence : 96466263

<220>
 <223> Distance between 3'-terminus of neighbour sequence of
 sequence listing upward to telomere on chosomal short arm and
 5'-terminus of this base sequence : 97275

<400> 912
 gacactcagc ctcacgagg atgcagagag aaaataactc gatggagaga agcaagcatt 60
 aggggggtta aatgaccagg ttggtggggg gaattaaatt atagacgggc ttaaaaaaca 120
 ggcaggggag gtttttctgt ttttgnctc gttttgtttt gttttgtttt gttttgtttt 180
 aaagacagga tcgcactctg ttgccagggc tggagtaca gggcaccaac atagctcact 240
 gtaacttcaa actccagga 259

Use of n and / or Xaa has been detected in the
 Sequence Listing. Review the Sequence Listing
 to ensure a corresponding explanation is present
 in the <220> to <223> fields of each sequence
 using n or Xaa.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/674,124DATE: 10/08/2003
TIME: 13:16:55

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

ase Note:

of n and/or Xaa have been detected in the Sequence Listing. Please review the
uence Listing to ensure that a corresponding explanation is presented in the <220>
<223> fields of each sequence which presents at least one n or Xaa.

#:28; N Pos. 34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53
#:28; N Pos. 54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73
#:28; N Pos. 74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93
#:28; N Pos. 94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109
#:28; N Pos. 110,111,112,113,114,115,116,117,118,119,120,121,122,123,124
#:28; N Pos. 125,126,127,128,129,130,131,132,133
#:863; N Pos. 94
#:912; N Pos. 147
#:3742; N Pos. 71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89
#:3742; N Pos. 90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106
#:3742; N Pos. 107,108,109,110,111,112,113,114,115,116,117,118,119,120
#:3742; N Pos. 121,122,123,124,125,126,127,128,129,130,131,132,133,134
#:3742; N Pos. 135,136,137,138,139,140,141,142,143,144,145,146,147,148
#:3742; N Pos. 149,150,151,152,153,154,155,156,157,158,159,160,161,162
#:3742; N Pos. 163,164,165,166,167,168,169,170
#:3745; N Pos. 143,144
#:3746; N Pos. 143,144
#:4010; N Pos. 207,211,212,214,216,243,245,247,249,254,256,258,263,265
#:4010; N Pos. 267,269,271,275,278
#:4931; N Pos. 181,231,233
#:4934; N Pos. 6
#:4935; N Pos. 198
#:4936; N Pos. 91,108
#:5073; N Pos. 298
#:5452; N Pos. 312
#:5742; N Pos. 331,339
#:5895; N Pos. 157,158,159,160,161,162,163,164,165,166,167,168,169,170
#:5895; N Pos. 171,172,173,174,175,176,177,178,179,180,181,182,183,184
#:5895; N Pos. 185,186,187,188,189,190,191,192,193,194,195,196,197,198
#:5895; N Pos. 199,200,201,202,203,204,205,206,207,208,209,210,211,212
#:5895; N Pos. 213,214,215,216,217,218,219,220,221,222,223,224,225,226
#:5895; N Pos. 227,228,229,230,231,232,233,234,235,236,237,238,239,240
#:5895; N Pos. 241,242,243,244,245,246,247,248,249,250,251,252,253,254
#:5895; N Pos. 255,256
#:5994; N Pos. 67
#:6080; N Pos. 393,449
#:6525; N Pos. 262,263,264,265,266,267,268,269,270,271,272,273,274,275
#:6525; N Pos. 276,277,278,279,280,281,282,283,284,285,286,287,288,289
#:6525; N Pos. 290,291,292,293,294,295,296,297,298,299,300,301,302,303
#:6525; N Pos. 304,305,306,307,308,309,310,311,312,313,314,315,316,317
#:6525; N Pos. 318,319,320,321,322,323,324,325,326,327,328,329,330,331
#:6525; N Pos. 332,333,334,335,336,337,338,339,340,341,342,343,344,345
#:6525; N Pos. 346,347,348,349,350,351,352,353,354,355,356,357,358,359
#:6525; N Pos. 360,361

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/674,124

DATE: 10/08/2003
TIME: 13:16:55

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

#:7259; N Pos. 59
#:7624; N Pos. 97,99
#:7989; N Pos. 71
#:8303; N Pos. 49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67
#:8303; N Pos. 68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86
#:8303; N Pos. 87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103
#:8303; N Pos. 104,105,106,107,108,109,110,111,112,113,114,115,116,117

alid <213> Response:

of "Artificial" only as "<213> Organism" response is incomplete,
1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

#:27089,27090,27091,27092,27093,27094,27095,27096,27097,27098,27099,27100
#:27101,27102,27103,27104,27105,27106,27107,27108,27109,27110

of <220> Feature (NEW RULES):

uence(s) are missing the <220> Feature and associated headings.

of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
Unknown". Please explain source of genetic material in <220> to <223>
tion (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
c.1.823 of new Rules)

#:27089,27090,27091,27092,27093,27094,27095,27096,27097,27098,27099,27100
#:27101,27102,27103,27104,27105,27106,27107,27108,27109,27110

VARIABLE LOCATION SUMMARY

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of n's or Xaa's (NEW RULES):

of n's and/or Xaa's have been detected in the Sequence Listing.

of <220> to <223> is MANDATORY if n's or Xaa's are present.

<220> to <223> section, please explain location of n or Xaa, and which idue n or Xaa represents.

#:28; N Pos. 34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53
#:28; N Pos. 54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73
#:28; N Pos. 74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93
#:28; N Pos. 94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109
#:28; N Pos. 110,111,112,113,114,115,116,117,118,119,120,121,122,123,124
#:28; N Pos. 125,126,127,128,129,130,131,132,133
#:863; N Pos. 94
#:912; N Pos. 147
#:3742; N Pos. 71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89
#:3742; N Pos. 90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106
#:3742; N Pos. 107,108,109,110,111,112,113,114,115,116,117,118,119,120
#:3742; N Pos. 121,122,123,124,125,126,127,128,129,130,131,132,133,134
#:3742; N Pos. 135,136,137,138,139,140,141,142,143,144,145,146,147,148
#:3742; N Pos. 149,150,151,152,153,154,155,156,157,158,159,160,161,162
#:3742; N Pos. 163,164,165,166,167,168,169,170
#:3745; N Pos. 143,144
#:3746; N Pos. 143,144
#:4010; N Pos. 207,211,212,214,216,243,245,247,249,254,256,258,263,265
#:4010; N Pos. 267,269,271,275,278
#:4931; N Pos. 181,231,233
#:4934; N Pos. 6
#:4935; N Pos. 198
#:4936; N Pos. 91,108
#:5073; N Pos. 298
#:5452; N Pos. 312
#:5742; N Pos. 331,339
#:5895; N Pos. 157,158,159,160,161,162,163,164,165,166,167,168,169,170
#:5895; N Pos. 171,172,173,174,175,176,177,178,179,180,181,182,183,184
#:5895; N Pos. 185,186,187,188,189,190,191,192,193,194,195,196,197,198
#:5895; N Pos. 199,200,201,202,203,204,205,206,207,208,209,210,211,212
#:5895; N Pos. 213,214,215,216,217,218,219,220,221,222,223,224,225,226
#:5895; N Pos. 227,228,229,230,231,232,233,234,235,236,237,238,239,240
#:5895; N Pos. 241,242,243,244,245,246,247,248,249,250,251,252,253,254
#:5895; N Pos. 255,256
#:5994; N Pos. 67
#:6080; N Pos. 393,449
#:6525; N Pos. 262,263,264,265,266,267,268,269,270,271,272,273,274,275
#:6525; N Pos. 276,277,278,279,280,281,282,283,284,285,286,287,288,289
#:6525; N Pos. 290,291,292,293,294,295,296,297,298,299,300,301,302,303
#:6525; N Pos. 304,305,306,307,308,309,310,311,312,313,314,315,316,317
#:6525; N Pos. 318,319,320,321,322,323,324,325,326,327,328,329,330,331
#:6525; N Pos. 332,333,334,335,336,337,338,339,340,341,342,343,344,345
#:6525; N Pos. 346,347,348,349,350,351,352,353,354,355,356,357,358,359

VARIABLE LOCATION SUMMARY

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Input Set : D:\seqlist.txt

Output Set: N:\CRF4\10082003\J674124.raw

#:6525; N Pos. 360,361

#:7259; N Pos. 59

#:7624; N Pos. 97,99

#:7989; N Pos. 71

#:8303; N Pos. 49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67

#:8303; N Pos. 68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86

#:8303; N Pos. 87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103

#:8303; N Pos. 104,105,106,107,108,109,110,111,112,113,114,115,116,117

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Output Set: N:\CRF4\10082003\J674124.raw

3 M:270 C: Current Application Number differs, Replaced Current Application Number
37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
41 Repeated in SeqNo=28
8637 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:863
8637 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:863
8637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:863 after pos.:60
0264 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:912
0264 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:912
0264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:912 after pos.:120
26228 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3742
26232 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3742
26235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3742 after pos.:60
41 Repeated in SeqNo=3742
26346 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3745
26346 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3745
26346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3745 after pos.:120
26383 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3746
26383 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3746
26383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3746 after pos.:120
35639 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4010
35639 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4010
35639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4010 after pos.:180
41 Repeated in SeqNo=4010
67364 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4931
67364 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4931
67364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4931 after pos.:180
67463 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4934
67463 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4934
67463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4934 after pos.:0
67504 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4935
67504 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4935
67504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4935 after pos.:180
67531 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4936
67531 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4936
67531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4936 after pos.:60
72172 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5073
72172 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5073
72172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5073 after pos.:240
85187 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5452
85187 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5452
85187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5452 after pos.:300
95157 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5742
95157 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5742
95157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5742 after pos.:300
00438 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5895
00438 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5895
00438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5895 after pos.:120

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41 Repeated in SeqNo=5895

03877 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5994

03877 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5994

03877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5994 after pos.:60

06835 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:6080

06835 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:6080

06835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6080 after pos.:360

41 Repeated in SeqNo=6080

21820 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:6525

21820 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:6525

21820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6525 after pos.:240

41 Repeated in SeqNo=6525

46228 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7259

46228 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7259

46228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7259 after pos.:0

58531 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7624

58531 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7624

58531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7624 after pos.:60

70586 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7989

70586 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7989

70586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7989 after pos.:60

81124 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:8303

81124 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8303

81124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8303 after pos.:0

41 Repeated in SeqNo=8303

96787 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:8774

96787 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8774

96787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8774 after pos.:240

07698 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9093

07698 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9093

07698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9093 after pos.:180

09191 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9138

09191 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9138

09191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9138 after pos.:240

52518 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13393

52518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13393 after pos.:360

53798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13431 after pos.:0

65508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13779 after pos.:120

69639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13900 after pos.:240

71026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13941 after pos.:0

71057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13942 after pos.:0

41 Repeated in SeqNo=13942

74427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14044 after pos.:0

78017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14148 after pos.:0

79327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14188 after pos.:0

80750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14231 after pos.:60

85639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14376 after pos.:0

41 Repeated in SeqNo=14376

89894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14501 after pos.:60

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92778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14587 after pos.:60
00166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14805 after pos.:0
00308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14809 after pos.:60
00817 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14824 after pos.:60